REMARKS

By this Office Action, the Examiner has required restriction to one of the following inventions:

I.   Claims 20-26, drawn to ONE isolated nucleic acid, a vector thereof, and cultured cell, classified in class 536, subclass 23.1; class 435, subclasses 69.1, 320.1, 325.
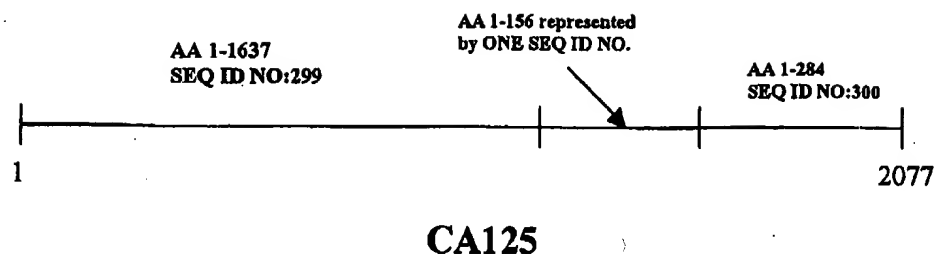
(Upon electrion of Group I above, Applicant must further elect ONE nucleic acid from those listed in Calim 20, part a, and ONE corresponding encloded polypeptide from those listed in Claim 21, part a, as each sequence represents a separate invention, not a species. Additionally, Claim 26 will only be examined to the extent it reads on the elected sequence(s).)

II.   Claims 14-19, 27, 30-33 drawn to ONE purified polypeptide, classified in class 530, subclass 350; class 424, subclass 184.1.

(Upon election of Group II above, Applicant must further elect ONE polypeptide sequence from those listed in Claim 27, part a, as each sequence represents a separate invention, not a species. Claims 14-19 will only be examined to the extent they read on the elected sequence.)

III.   Claims 1-12, drawn to ONE CA125 molecule comprising an extracellular domain of SEQ ID NO.: 299, ONE repeat domain, and ONE cytoplasmic domain comprising SEQ ID NO.: 300, classified in class 530, subclass 350.

(Upon election of Group III, Applicant must further elect ONE multiple repeat domain corresponding to ONE linear sequence identifier comprising smino acids 1-156 of domains 1-5. For example, upon election, of Group III, a search and examination of a 2077 AA polypeptide will take place as set forth below:

AA 1-1637
SEQ ID NO:299

AA 1-156 represented
by ONE SEQ ID NO.

AA 1-284
SEQ ID NO:300

|————————————————————|————————⟍—————|————————————|

1   2077

CA125

IV.   Claim 13, drawn to a CA125 molecule comprising SEQ ID NO.: 162, classified in class 530, subclass 350.

V.   Claims 28-29 drawn to a purified antibody that binds to ONE polypeptide, classified in class 530, subclass 387.1.

(Upon election of Group V above, Applicant must further elect ONE polypeptide sequence from those listed in Claim 28, part a, as each sequence represents a separate invention, not a species.)

VI.   Claim 34, drawn to ONE antisense molecule, classified in class 800, subclass 286.

(Upon election of Group VI above, Applicant must further elect ONE nucleic acid from those listed in Claim 20, part a, as each sequence represents a separate invention, not a species.)

Responsive to the Requirement for restriction, Applicant elects to prosecute the invention of group III, with traverse Claims 1-12 drawn to one polypeptide. The applicant elects the repeat domain as shown in SEQ ID NO. 150 for examination.

Applicants respectfully request reconsideration of the Requirement for Restriction, or in the alternative, modification of the Restriction Requirement to allow prosecution of more than one group of Claims designated by the Examiner in the present Application, for the reasons provided as follows.

Under 35 U.S.C § 121 "two or more independent and distinct inventions . . . in one Application may . . . be restricted to one of the inventions." Inventions are "independent" if "there is no disclosed relationship between the two or more subjects disclosed" (MPEP 802.01).

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The term "distinct" means that "two or more subjects as disclosed are related . . . but are capable of separate manufacture, use or sale as claimed, AND ARE PATENTABLE OVER EACH OTHER" (MPEP 802.01) (emphasis in original). However, even with patentably distinct inventions, restriction is not required unless one of the following reasons appear (MPEP 808.02):

1. Separate classification

2. Separate status in the art; or

3. Different field of search.

Further, under patent Office Examining Procedures, "[i]f the Search and Examination of an entire Application can be made without serious burden, the Examiner must examine it on the merits, even though it includes claims to distinct or independent inventions" (MPEP 803, Rev. 8, May 1988) (emphasis added).

The Examiner's assertions to the contrary notwithstanding, Applicants respectfully submit that conjoint examination and inclusion of all of the Clams of the present Application would not present an undue burden on the Examiner, and accordingly, withdrawal of the Requirement for Restriction.

With respect to the requirement to elect a single species for examination on the merits, Applicants respectfully traverse this requirement for the following reasons:

I.   Claim 1(b) providing the multiple repeat domains does not include a genus species relationship

Claim 1(b) relates to a multiple repeat domain. A CA125 molecule can include a variety, if not all of the repeats in a single molecule. SEQ ID NO: 162 which show the recombinant molecule has been marked up as Appendix Tab A, to show the multiple repeats present in a single molecule. Claims to be restricted to different species must be mutually exclusive. The general test as to when claims are restricted respectively to different species is the fact that one claim recites limitations which under the disclosure are found in a first species, but not in a second, while a second claim recites limitations disclosed only from the second species and not the first. MPEP § 12.0[3[c]. As can be seen from an inspection of the recombinant molecule shown in SEQ ID NO: 162, CA125 molecule within the scope of claim 1(b) may have multiple

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repeat domains which are not mutually exclusive. Consequently, Applicants respectfully request examination on the multiple repeat domains as claimed. This requirement to elect a single combination of repeats violates the basic right of the Applicants to claim his invention as he chooses. In re Weber, 580 F.2d 455 (USCC 1978).

II.   Restriction is not appropriate if the claims are directed to substantially the same molecule
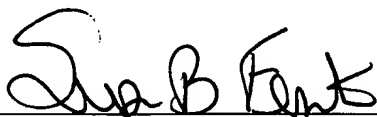
Species are patentably distinct when they are related, but they are capable of separate manufacture and are patentable (novel and nonobvious) over each other. The multiple repeat domains contain multiple repeats wherein each repeat unit has five genomic exons. The variation in repeats set out in Claim 1 (b) are 82% identical and thus present related chemical compounds. The repeat domain is a sequence of 156 amino acids which are repeated multiple times within a discrete portion of the CA125 protein. The repeat domain has its own function and combines with the other domains to provide the overall function of the protein. The designated exons in the repeat domain can vary, but, this variance is minimal. Importantly, when the nucleic acids are expressed they form a CA125 protein. Restriction is not appropriate if claims are directed to the same protein.

In view of the above, withdrawal of the Requirement for the Restriction is requested, and an early action on the merits of the Claims is courteously solicited.

Respectfully Submitted,

BUTLER, SNOW, O'MARA,
STEVENS & CANNADA
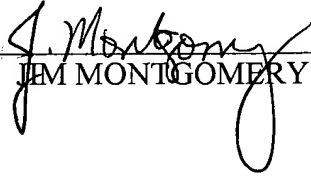
Date: 10-5-05   By: _____

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JIM MONTGOMERY

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```
A  TVPFMVPFTL  NFTITNLQYE  EDMRHPGSRK
                164

  12101   FNATERELQG  ILKPLFRNSS  LEYLYSGCRL  ASLRPEKDSS  AMAVDAICTH
                                   195

  12151   RPDPEDLGLD  RERLYWELSN  LTNGIQELGP  YTLDRNSLYV  NGFTHRSSMP
                222                                        250

  12201   TTSTPGTSTV  DVGTSGTPSS  SPSPT██████████████████████████
               278                            171

  12251   ███████████████████████████████████████████████████████

  12301   ███████████████████████████████████████████████████████

  12351   ███████████████████████ SGTESSLSSP  TLMAAGPLLV  PFTLNFTITN
                                     219

  12401   LQYGEDMGHP  GSRKFNTTER  VLQGILGPIF  KNTSVGPLYS  GCRLTSLRSE
                                                            201

  12451   KDGAATGVDA  ICIHHLDPKS  PGLNRERLYW  ELSQLTNGIK  ELGPYTLDRN
                        234

  12501   SLYVNGFTHR  TSVPTSSTPG  TSTVDLGTSG  TPFSLPSPAT  AGPLVPFTL
                        252           280

  12551   ████████████ EDMHRPGSRK  FNTTERVLQG  ILGPMFKNTS  VGLDYSGCRL
                 170                                        202

  12601   ████████████████████████████████████████████████████████
                                  235

  12651   ████████████████████ TSSTPGTSTV  DLGSGTPSSL  PSPTAAGPLL
                                  267              281

  12701   VPFTLNFTIT  NLQYEEDMHH  PGSRKFNTTE  RVLQGILGPM  FKNTSVGLLY
                182                                        202

  12751   SGCRLTLLRS  EKDGAATGVD  AICTHRLDPK  SPGVDREQLY  WELSQLTNGI
                        236

  12801   KELGPYTLDR  NSLYVNGFTH  QTSAPNTSTP  GTSTVDLGTS  GTPSSLPSPT
                        263           283

  12851   ████████████████████████████████████████████████████████
                   170

  12901   ████████████████████████████████████████████████████████
                146                   236

  12951   ████████████████████████████████████████████████████████
                                   263           283

  13001   ████SAGP  LLVPFTLNFT  ITNLQYEEDM  HHPGSRKFNT  TERVLQGILG
               183

  13051   PMFKNTSVGL  LYSGCRLTLL  RPEKNGAATG  MDAICSHRLD  PKSPGLNREQ
               202                     240

  13101   LYWELSQLTH  GIKELGPYTL  DRNSLYVNGF  THRSSVAPTS  TPGTSTVDLG
                                              254

  13151   TSGTPSSLPS  PTT████████████████████████████████████████
               283                   165

  13201   ████████████████████████████████████████████████████████
                        205

  13251   ████████████████████████████████████████████████████████

  13301   ████████████TA  GPLLVPFTLN  FTITNLQYEE  DMHRPGSRKF
                                         171

  13351   NATERVLQGL  LSPIFKNSSV  GPLYSGCRLT  SLRPEKDGAA  TGMDAVCLYH
                        207

  13401   PNPKRPGLDR  EQLYWELSQL  THNITELGPY  SLDRDSLYVN  GFTHQNSVPT
               227                                        265

  13451   TSTPGTSTVY  WATTGTPSSF  PGHTEPGPLL  IPFTFNFTIT  NLHYEENMQH
               286                             180
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                                          200
13501  PGSRKFNTTE  RVLQGILKPL  FKNTSVGPLY  SGCRLTSLRP  EKDGAATGMD
                228
13551  AVCLYHPNPK  RPGLDREQLY  CELSQLTHNI  TELGPYSLDR  DSLYVNGFTH
       205            280                              186
13601  QNSVPTTSTP  GTSTVYWATT  GTPSSFPGHT |EPGPLLIPFT  FNFTITNLHY
                                            197
13651  EENMQHPGSR  KFNTTERVLQ  GILKPLFKNT  SVGPLYSGCR  LTLLRPEKHE
                       244
13701  AATGVDTICT  HRVDPIGPGL  DRERLYWELS  QLTNSITELG  PYTLDRDSLY
           271                      287
13751  VNGFNPRSSV  PTTSTPGTST  VHLATSGTPS  SLPGRTAPVP  LIIPFTLNFT
              188                                   197
13801  ITNLHYEENM  QHPGSRKFNT  TERVLQGILR  PLFKNTSVGP  LYSGCRLTLL
                                             2
13851  RPEKHEAATG  VDTICTHRVD  PIGPGLDREX  LYWELSXLTX  XIXELGPYXL
                     2                      2
13901  DRXSLYVNGF  XXXXXXXXTS  TPGTSXVXLX  TSGTPXXXPX  XTSAGPLLVP
              183                             202
13951  FTLNFTITNL  QYEEDMHHPG  SRKFNTTERV  LQGILGPMFK  NTSVGLLYSG
                                 241
14001  CRLTLLRPEK  MGAATGMDAV  CYHRLDPKSP  GLDREQLYWE  LSQLTHLIXE
                     250                      283
14051  LGPYTLDRNS  LYVNGFTHRS  SVAPTSTPGT  STVDLGTSGT  PSSLPSPTTA
              165
14101  VPLLVPFTLN  FTITNLQYGE  DMRHPGSRKF  NTTERVLQGL |LGPLFKNSSV
       205                         238
14151  GPLYSGCRLI  SLRSEKDGAA  TGVDAICTHH  LNPQSPGLDR  EQLYWQLSQM
                            257           285
14201  TNGIKELGPY  TLDRNSLYVN  GFTHRSSGLT  TSTPWTSTVD  LGTSGTPSPV
                        177
14251  PSPTTAGPLL  VPFTLNFTIT  NLQYEEDMHR  PGSRKFNATE  RVLQGILSPI
       207                         227
14301  FKNSSVGPLY  SGCRLTSLRP  EKDGAATGMD  AVCLYHPNPK  RPGLDREQLY
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14351  WELSQLTHNI  TELGPYSLDR  DSLYVNGFTH  QSSMTTTRTP  DTSTMHLATS
       289                      172
14401  RTPASLSGPT |TASPLLVLFT  INCTITNLQY  EEDMRRTGSR  KFNTMESVLQ
              197                      224
14451  GILKPLFKNT  SVGPLYSGCR  LTLLRPKKDG  AATGVDAICT  HRLDPKSPGL
                                      262
14501  NREQLYWELS  KLTNDIEELG  PYTLDRNSLY  VNGFTHQSSV  STTSTPGTST
              279                 2
14551  VDLRTSGTPS  SLSSPTIMXX  XPLLXPFTLN  FTITNLXYEE  XMXXPGSRKF
                                210
14601  NTTERVLQGL |LRPLFKNTSV  SSLYSGCRLT  LLRPEKDGAA  TRVDAACTYR
              224                                      271
14651  PDPKSPGLDR  EQLYWELSQL  THSTTELGPY  TLDRVSLYVN  TFNPRSSVPT
              287
14701  TSTPGTSTVH  LATSGTPSSL  PGHTXXXPLL  XPFTLNFTIT  NLXYEEXMXX
                                      195
14751  PGSRKFNTTE  RVLQGILKPL  FRNSSLEYLY  SGCRLASLRP  EKDSSAMAVD
                       222
14801  AICTHRPDPE  DLGLDRERLY  WELSNLTNGI  QELGPYTLDR  NSLYVNGFTH
       259            285
14851  RSSFLTTSTP  WTSTVDLGTS  GTPSPVPSPT |TAGPLLVPFT  LNFTITNLQY
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16351   NGAATGMDAI CTHRLDPKSP GLDREXLYWE LSXLTXXIXE LGPYXLDRXS ----
16401   LYVNGFXXXX XXXXTSTPGT SXVXLXTSGT PXXXPXXTXX XPLLXPFTLN
16451   FTITNLXYEE XMXXPGSRKF NTTERVLQGL LKPLFRNSSL EYLYSGCRLA
16501   SLRPEKDSSA MAVDAICTHR PDPEDLGLDR ERLYWELSNL TNGIQELGPY
16551   TLDRNSLYVN GFTHRSSMPT TSTPGTSTVD VGTSGTPSSS PSPTTAGPLL
16601   IPFTLNFTIT NLQYGEDMGH PGSRKFNTTE RVLQCILCPI FKNTSVGPLY
16651   SGCRLTSLRS EKDGAATGVD AICIHHLDPK SPGLNRERLY WELSQLTNGI
16701   KELGPYTLDR NSLYVNGFTH RTSVPTTSTP GTSTVDLGTS GTPFSLPSPA
16751   TAGPLLVLFT LNFTITNLKY EEDMHRPGSR KFNTTERVLQ TILGPMFKNT
16801   SVGLLYSGCR LTLLRSEKDG AATGVDAICT HRLDPKSPGL DREXLYWELS
16851   XLTXXIXELG PYXLDRXSLY VNGFXXXXXX XXTSTPGTSX VXLXTSGTPX
16901   XXPXXTXXXP LLXPFTLNFT ITNLXYEEXM XXPGSRKFNT TERVLQGLLR
16951   PVFKNTSVGP LYSGCRLTLL RPKKDGAATK VDAICTYRPD PKSPGLDREQ
17001   LYWELSQLTH SITELGPYTQ DRDSLYVNGF THRSSVPTTS IPGTSAVHLE
17051   TTGTPSSFPG HTEPGPLLIP FTFNFTITNL RYEENMQHPG SRKFNTTERV
17101   LQGILTPLFK NTSVGPLYSG CRLTLLRPEK QEAATGVDTI CTHRVDPIGP
17151   GLDRERLYWE LSQLTNSITE LGPYTLDRDS LYVDFNPWS SVPTTSTPGT
17201   STVHLATSGT PSPLPGHTAP VPLLIPFTLN FTITDLHYEE NMQHPGSRKF
17251   NTTERVLQGL LKPLFKSTSV GPLYSGCRLT LLRPEKHGAA TGVDAICTLR
17301   LDPTGPGLDR ERLYWELSQL TNSITELGPY TLDRDSLYVN GFNPWSSVPT
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17401   PGSRKFNTTE RVLQSLHGPM FKNTSVGPLY SGCRLTLLRS EKDGAATGVD
17451   AICTHRLDPK SPGLDREXLY WELSXLTXXI XELGPYXLDR XSLYVNGFXX
17501   XXXXXTSTIP GTSXVXLXTS GTPXXXPXXT XXXPLLXPFT LNFTITNLXY
17551   EEXMXXPGSR KFNTTERVLQ GILXPXFKXT SVGXLYSGCR LTLLRXEKXX
17601   AATXVDXXCX XXXDPXXPGL DREXLYWELS XLTNSITELG PYTLDRDSLY
17651   VNGFTHRSSM PTTSIPGTSA VHLETSGTPA SLPGHTAPGP LLVPFTLNFT
17701   ITNLQYEEDM RHPGSRKFNT TERVLQGILK PLFKSTSVGP LYSGCRLTLL
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2.

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                         1
17851  FTLNFTITNL  XYEEXMXXPG  SRKFNTTERV  LQGILXPXFK  XTSVGXLYSG
                                            1                      1
17901  CRLTLLRXEK  XXAATXVDXX  CXXXXDPXXP  GLDREXLYWE  LSXLTXXIXE
                         270         287
17951  LGPYXLDRXS  LYVNGFHPRS  SVPTTSTPGT  STVHLATSGT  PSSLPGHTAP
                  188
18001  VPLLIPFTLN  FTITNLHYEE  NMQHPGSRKF  NTTERVLQGL| LGPMFKNTSV
       202                                 1
18051  GLLYSGCRLT  LLRPEKNGAA  TGMDAICSHR  LDPKSPGLDR  EXLYWELSXL
                                 1                          1
18101  TXXIXELGPY  XLDRXSLYVN  GFXXXXXXXX  TSTPGTSXVX  LXTSGTPXXX
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18151  PXXTXXXPLL  XPFTLNFTIT  NLXYEEXMXX  PGSRKFNTTE  RVLQGILXPX
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18201  FKXTSVGXLY  SGCRLTLLRX  EKXXAATXVD  XXCXXXXDPX  XPGLDREXLY
                              265        286
18251  WELSXLTXXI  XELGPYXLDR  XSLYVNGFTH  QNSVPTTSTP  GTSTVYWATT
                                186
18301  GTPSSFPGHT| EPGPLLIPFT  FNFTITNLHY  EENMQHPGSR  KFNTTERVLQ
              218
18351  GILTPLFKNT  SVGPLYSGCR  LTLLRPEKQE  AATGVDTICT  HRVDPIGPGL
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18401  DREXLYWELS  XLTXXIXELG  PYXLDRXSLY  VNGFXXXXXX  XXTSTPGTSX
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18451  VXLXTSGTPX  XXPXXTXXXP  LLXPFTLNFT  ITNLXYEEXM  XXPGSRKFNT
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18501  TERVLQGILX  PXFKXTSVGX  LYSGCRLTLL  RXEKXXAATX  VDXXCXXXXD
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18551  PXXPGLDREX  LYWELSXLTX  XIXELGPYXL  DRXSLYVNGF  THRSSVPTTS
              287                          188
18601  SPGTSTVHLA  TSGTPSSLPG  HTAPVPLLIP  FTLNFTITNL  HYEENMQHPG
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18651  SRKFNTTERV  LQGLLKPLFK  STSVGPLYSG  CRLTLLRPEK  HGAATGVDAI
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18701  CTLRLDPTGP  GLDREXLYWE  LSXLTXXIXE  LGPYXLDRXS  LYVNGFXXXX
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18751  XXXXTSTPGT  SXVXLXTSGT  PXXXPXXTXX  XPLLXPFTLN  FTITNLXYEE
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18801  XMXXPGSRKF  NTTERVLQGL| LXPXFKXTSV  GXLYSGCRLT  LLRXEKXXAA
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18851  TXVDXXCXXX  XDPXXPGLDR  EXLYWELSXL  TXXIXELGPY  XLDRXSLYVN
       253                     287
18901  GFTHRTSVPT  TSTPGTSTVH  LATSGTPSSL  PGHTAPVPLL  IPFTLNFTIT
       180                                 207
18951  NLQYEEDMHR  PGSRKFNTTE  RVLQGILSPI  FKNSSVGPLY  SGCRLTSLRP
              228
19001  EKDGAATGMD  AVCLYHPNPK  RPGLDREQLY  CELSQLTHNI  TELGPYSLDR
                   265                     286
19051  DSLYVNGFTH  QNSVPTTSTP  GTSTVYWATT  GTPSSFPGHT| XXXPLLXPFT
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19101  LNFTITNLXY  EEXMXXPGSR  KFNTTERVLQ  GILXPXFKXT  SVGXLYSGCR
                   1
19151  LTLLRXEKXX  AATXVDXXCX  XXXDPXXPGL  DREXLYWELS  XLTXXIXELG
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19201   PYXLDRXSLY  VNGFTHWSSG  LTTSTPWTST  VDLGTSGTPS  PVPSPTTAGP
                         269             285
19251   LLVPFTLNFT  ITNLQYEEDM  HRPGSRKFNA  TERVLQGILS  PIFKNTSVGP
                    177
19301   LYSGCRLTLL  RPEKQEAATG  VDTICTHRVD  PIGPGLDREX  LYWELSXLTX
        208                               2
19351   XIXELGPYXL  DRXSLYVNGF  XXXXXXXXTS  TPGTSXVXLX  TSGTPXXXPX
                         2                 7
19401   XTXXXPLLXP  FTLNFTITNL  XYEEXMXXPG  SRKFNTTERV  LQGILXPXFK
             2                               2
19451   XTSVGXLYSG  CRLTLLRXEK  XXAATXVDXX  CXXXXDPXXP  GLDREXLYWE
             2                               2
19501   LSXLTXXIXE  LGPYXLDRXS  LYVNGFTHRS  FGLTTSTPWT  STVDLGTSGT
                                   258         285
19551   PSPVPSPTTA  GPLLVPFTLN  FTITNLQYEE  DMHRPGSRKF  NTTERVLQGL
                                179
19601   LTPLFRNTSV  SSLYSGCRLT  LLRPEKDGAA  TRVDAVCTHR  PDPKSPGLDR
             219          2
19651   EXLYWELSXL  TXXIXELGPY  XLDRXSLYVN  GFXXXXXXXX  TSTPGTSXVX
             2                           2        2
19701   LXTSGTPXXX  PXXTXXXPLL  XPFTLNFTIT  NLXYEEXMXX  PGSRKFNTTE
             2           2                 2
19751   RVLQGILXPX  FKXTSVGXLY  SGCRLTLLRX  EKXXAATXVD  XXCXXXXDPX
             2               2        2
19801   XPGLDREXLY  WELSXLTXXI  XELGPYXLDR  XSLYVNGFTH  WIPVPTSSTP
        281                               267
19851   GTSTVDLGSG  TPSSLPSPTT  AGPLLVPFTL  NFTITNLQYG  EDMGHPGSRK
                                         175
19901   FNTTERVLQG  ILGPIFKNTS  VGPLYSGCRL  TSLRSEKDGA  ATGVDAICIH
                    201      2
19951   HLDPKSPGLD  REXLYWELSX  LTXXIXELGP  YXLDRXSLYV  NGFXXXXXXX
             2                                           7
20001   XTSTPGTSXV  XLXTSGTPXX  XPXXTXXXPL  LXPFTLNFTI  TNLXYEEXMX
             7        2
20051   XPGSRKFNTT  ERVLQGILXP  XFKXTSVGXL  YSGCRLTLLR  XEKXXAATXV
                         7                 7
20101   DXXCXXXXDP  XXPGLDREXL  YWELSXLTXX  IXELGPYXLD  RXSLYVNGFT
20151   HQTFAPNTST  PGTSTVDLGT  SGTPSSLPSP  TSAGPLLVPF  TLNFTITNLQ
        264             283
20201   YEEDMHHPGS  RKFNTTERVL  QGILGPMFKN  TSVGLLYSGC  RLTLLRPEKN
             183                    2         202
20251   GAATRVDAVC  THRPDPKSPG  LDREXLYWEL  SXLTXXIXEL  GPYXLDRXSL
20301   YVNGFXXXXX  XXXTSTPGTS  XVXLXTSGTP  XXXPXXTAPV  PLLIPFTLNF
             2           7                 2
20351   TITNLHYEEN  MQHPGSRKFN  TTERVLQGIL  RPLFKSTSVG  PLYSGCRLTL
             188                                   213
20401   LRPEKHGAAT  GVDAICTLRL  DPTGPGLDRE  RLYWELSQLT  NSVTELGPYT
                    242
20451   LDRDSLYVNG  FTQRSSVPTT  SIPGTSAVHL  ETSGTPASLP  GHTAPGPLLV
                    273                 290
20501   PFTLNFTITN  LQYEVDMRHP  GSRKFNTTER  VLQGILKPLF  KSTSVGPLYS
             169                                   198
20551   GCRLTLLRPE  KRGAATGVDT  ICTHRLDPLN  PGLDREQLYW  ELSKLTRGII
                                         239
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20601  ELGPYLLDRG  SLYVNGFTHR  NFVPITSTPG  TSTVHLGTSE  TPSSLPRPIV
                            260                    292
20651  PGPLLVPFTL  NFTITNLQYE  EAMRHPGSRK  FNTTERVLQG  ILRPLFKNTS
                  166
20701  IGPLYSSCRL  TLLRPEKDKA  ATRVDAICTH  HPDPQSPGLN  REQLYWELSQ
       212                                247
20751  LTHGITELGP  YTLDRDSLYV  DGFTHWSPIP  TTSTPGTSIV  NLGTSGIPPS
                               268                          293
20801  LPETTXXXPL  LXPFTLNFTI  TNLXYEEXMX  XPGSRKFNTT  ERVLQGILKP
                    2
20851  LFKSTSVGPL  YSGCRLTLLR  PEKDGVATRV  DAICTHRPDP  KIPGLDRQQL
            198                                   233
20901  YWELSQLTHS  ITELGPYTLD  RDSLYVNGFT  QRSSVPTTST  PGTFTVQPET
                                        274
20951  SETPSSLPGP  TATGPVLLPF  TLNFTITNLQ  YEEDMHRPGS  RKFNTTERVL
       294                               181
21001  QGILMPLFKN  TSVSSLYSGC  RLTLLRPEKD  GAATRVDAVC  THRPDPKSPG
                 220
21051  LDRERLYWKL  SQLTHGITEL  GPYTLDRHSL  YVNGFTHQSS  MTTTRTPDTS
                 232                             266
21101  TMHLATSRTP  ASLSGPTTAS  PLLVLFTINF  TITNLRYEEN  MHHPGSRKFN
          289                                185
21151  TTERVLQGIL  RPVFKNTSVG  PLYSGCRLTL  LRPKKDGAAT  KVDAICTYRP
                          215
21201  DPKSPGLDRE  QLYWELSQLT  HSITELGPYT  QDRDSLYNVG  FTQRSSVPTT
               231                                  275
21251  SVPGTPTVDL  GTSGTPVSKP  GPSAASPLLV  LFTLNGTITN  LRYEENMQHP
             295                            190
21301  GSRKFNTTER  VLQGILRSLF  KSTSVGPLYS  GCRLTLLRPE  KDGTATGVDA
                          216
21351  ICTHHPDPKS  PRLDREQLYW  ELSQLTHNIT  ELGHYALDND  SLFVNGFTHR
                 225
21401  SSVSTTSTPG  TPTVYLGASK  TPASIFGPSA  ASHLLILFTL  NFTITNLRYE
       255           296                                192
21451  ENMWPGSRKF  NTTERVLQGL  LRPLFKNTSV  GPLYSGSRLT  LLRPEKDGEA
                               211
21501  TGVDAICTHR  PDPTGPGLDR  EQLYLELSQL  THSITELGPY  TLDRDSLYVN
                            226
21551  GFTHRSSVPT  TSTGVVSEEP  FTLNFTINNL  RYMADMGQPG  SLKFNITDNV
       254                             193
21601  MKHILSPLFQ  RSSLGARYTG  CRVIALRSVK  NGAETRVDLL  CTYLQPLSGP
                    209
21651  GLPIKQVFHE  LSQQTHGITR  LGPYSLDKDS  LYLNGYNEPG  LDEPPTTPKP
       297          248                       276
21701  ATTFLPPLSE  ATTAMGYHLK  TLTLNFTISN  LQYSPDMGKG  SATFNSTEGV
                               194
21751  LQHLIRPLFQ  KSSMGPFYLG  CQLISLRPEK  DGAATGVDTT  CTYHPDPVGP
              221
21801  GLDIQQLYWE  LSQLTHGVTQ  LGFYVLDRDS  LFINGYAPQN  LSIRGEYQIN
       249                               144
21851  FHIVNWNLSN  PDPTSSEY
       298
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